

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:27:19 ; Search time 65 Seconds
(without alignments)
54.271 Million cell updates/sec

Title: US-10-786-774-16
Perfect score: 28
Sequence: 1 DKCLA 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	39.3	5	1 AP21_EISFO	P84182 eisenia foe
2	7	25.0	5	1 TRAM3_ECOLI	P13973 escherichia
3	6	21.4	5	1 BIOA_CITFR	P13071 citrobacter
4	6	21.4	5	1 BIOB_CITFR	P12997 citrobacter
5	6	21.4	5	1 MPAJ1_JUNVI	P81826 juniperus v
6	6	21.4	5	1 RBE11_LITRU	P82070 litorea rub
7	6	21.4	5	1 UKA4_CHLTR	P38005 chlamydia t
8	6	21.4	5	2 Q99007_HORVU	Q99007 hordeum vul
9	6	21.4	5	2 P83073_BACCE	P83073 bacillus ce
10	5	17.9	5	1 BPP7_BOTIN	P30425 bothrops in
11	4	14.3	5	1 ALL14_CARMA	P81817 carcinus ma
12	4	14.3	5	1 FARP_CHICK	P83308 gallus gall
13	4	14.3	5	1 PRCT_CARMA	P67857 carcinus ma
14	4	14.3	5	1 PRCT_LIMPO	P67858 limulus pol
15	4	14.3	5	1 PRCT_PERAM	P67859 periplaneta
16	4	14.3	5	1 RBE21_LITRU	P82071 litorea rub
17	4	14.3	5	1 RPC2_EBP21	P69203 bacterioph
18	4	14.3	5	1 SUGA_ACHDO	P19991 acheta dome
19	2	7.1	5	1 E103_LITRU	P82099 litorea rub
20	2	7.1	5	1 E104_LITRU	P82100 litorea rub
21	2	7.1	5	1 FARP_ARTTR	P41853 artiopesthi
22	2	7.1	5	1 PSK_DAUCA	P58261 daucus caro
23	2	7.1	5	1 RBE31_LITRU	P82072 litorea rub
24	2	7.1	5	1 UC22_MAIZE	P80628 zea mays (m
25	2	7.1	5	1 UF01_MOUSE	P38639 mus musculu
26	1	3.6	5	1 RBE32_LITRU	P82073 litorea rub
27	1	3.6	5	1 TPIS_CANFA	P54714 canis fami
28	0	0.0	5	1 PAP2_PARMA	P81864 pardachirus

ALIGNMENTS

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RESULT 1
AP21_EISFO STANDARD; PRT; 5 AA.
AC P84182;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DB Antimicrobial peptide OSP121.
OS Eisenia foetida (Common branding worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RX PubMed=15253156;
RA Liu Y.-Q., Sun Z.-J., Wang C., Li S.-J., Liu Y.-Z.;
RT "Purification of a novel antibacterial short peptide in earthworm
RT Eisenia foetida.";
RL Acta Biochim. Biophys. Sin. 36:297-302(2004).
CC -|- FUNCTION: Displays antimicrobial activity against E.coli, S.aureus
CC and P.aeruginosa.
CC -|- MASS SPECTROMETRY: MW=510.8; METHOD=MALDI; RANGE=1-5; NOTE=Ref.1.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
KW Antibiotic; Antimicrobial; Direct protein sequencing.
SQ SEQUENCE 5 AA; 407 MW; 687DC5BEDB00000 CRC64;

Query Match 39.3%; Score 11; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CLA 5
Db 2 CSA 4

RESULT 2
TRAM3_ECOLI STANDARD; PRT; 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DB TraM protein (Fragment).
GN Namestram;
OS Escherichia coli.
OG Plasmid IncFII R100 (NR1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=88227859; PubMed=2836369;
RA Inamoto S., Yoshioka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the traJ and
RT traY genes of plasmid R100.";
RL J. Bacteriol. 170:2749-2757(1988).
CC -|- FUNCTION: Transfer gene protein. Is involved in the conjugation
CC process of bacterial cells for the exchange of plasmid DNA.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: Belongs to the traM family.
CC -----
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CC removed.
CC -----
DR ENBL; M20941; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR PIR; A32014; A32014.
DR Conjugation; DNA-binding; Plasmid.
FT NON TER 1
SQ SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;

Query Match 25.0%; Score 7; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
   |
Db 3 DE 4

RESULT 3
BIOB_CITFR STANDARD; PRT; 5 AA.
AC P13071;
P 01-JAN-1990 (Rel. 13, Created)
13-SEP-2005 (Rel. 48, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN Name=bioA;
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=8906280; PubMed=2971595; DOI=10.1016/0378-1119(88)90397-6;
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminononanoate.
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- PATHWAY: Cofactor biosynthesis; biotin biosynthesis; biotin from
CC 6-carboxyhexanoyl-CoA: step 2.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
CC aminotransferase family.
CC -----
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CC removed.
CC -----
DR ENBL; M21922; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR PIR; I40697; I40697.
DR InterPro; IPR005814; Aminotrans_3.
DR PROSITE; PS00600; AA TRANSFER CLASS 3; PARTIAL.
DR Aminotransferase; Biotin biosynthesis; Pyridoxal phosphate;
KW Aminotransferase.
FT NON TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 21.4%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 D 1
   |
Db 4 D 4

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RESULT 4
BIOB_CITFR STANDARD; PRT; 5 AA.
AC P12957;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).
GN Name=bioB;
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=89006280; PubMed=2971595; DOI=10.1016/0378-1119(88)90397-6;
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
CC -1- COFACTOR: Binds 1 4Fe-4S cluster coordinated with 3 cysteines and
CC an exchangeable S-adenosyl-L-methionine (By similarity).
CC -1- COFACTOR: Binds 1 2Fe-2S cluster coordinated with 3 cysteines and
CC 1 arginine (By similarity).
CC -1- PATHWAY: Cofactor biosynthesis; biotin biosynthesis; biotin from
CC 6-carboxyhexanoyl-CoA: step 4 [final step].
CC -1- SIMILARITY: Belongs to the biotin and lipoic acid synthetases
CC family.
CC -----
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CC removed.
CC -----
DR ENBL; M21922; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR PIR; I40698; I40698.
DR 2Fe-2S; 4Fe-4S; Biotin biosynthesis; Iron; Iron-sulfur; Metal-binding;
KW Transferase.
FT NON TER 5
SQ SEQUENCE 5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;

Query Match 21.4%; Score 6; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LA 5
   |
Db 1 MA 2

RESULT 5
MPAJ4 JUNVI STANDARD; PRT; 5 AA.
AC P81826;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Major pollen allergen Jun v 4 (Fragment).
OS Juniperus virginiana (Eastern red cedar).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Juniperus.
OX NCBI_TaxID=39584;
RN [1]
RP PROTEIN SEQUENCE, AND ALLERGENIC PROPERTIES.
RX TISSUE=Pollen;
RX MEDLINE=21315424; PubMed=11422137;
RX DOI=10.1046/j.1365-2222.2001.01079.x;
RA Midoro-Horiuti T., Goldblum R.M., Brooks E.G.;
RT "Identification of mutations in the genes for the pollen allergens of
RT eastern red cedar (Juniperus virginiana).";
RL Clin. Exp. Allergy 31:771-778(2001).

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CC -I- ALLERGEN: Causes an allergic reaction in human. Binds to IgE of
CC patients who are allergic to J. ashei.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Allergen; Direct protein sequencing.
KW STRAIN=L2/434/Bu;
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 491 MW; 75B33DDAADB000000 CRC64;

Query Match 21.4%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 D 1
Db 2 D 2

RESULT 6
RBE11_LITRU STANDARD; PRT; 5 AA.
AC P82070;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Rubellidin-1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RC Tissue=Skin secretion;
RA Steinbörner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians."
RL Aust. J. Chem. 49:955-963(1996).
CC -I- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -I- MASS SPECTROMETRY: MW=598; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A000000 CRC64;

Query Match 21.4%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 D 1
Db 2 D 2

RESULT 7
UXA4_CHLTR STANDARD; PRT; 5 AA.
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to Swiss-Prot.
CC -I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.5, its MW is: 28 kDa.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Siena-2DPAGE; P38005; -.
KW Direct protein sequencing.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 476 MW; 75BAA865AA8000000 CRC64;

Query Match 21.4%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 D 1
Db 4 D 4

RESULT 8
Q99007_HORVU PRELIMINARY; PRT; 5 AA.
AC Q99007;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Alpha amylase (Fragment).
GN Name=Amyl gene;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimaeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers."
RL Plant Mol. Biol. 16:713-724(1991).
DR EMBL; X54643; CAA38455.1; -; Genomic DNA.
FT CHAIN 1 5
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F000000 CRC64;

Query Match 21.4%; Score 6; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2
Db 3 NK 4

RESULT 9


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CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 5 5 Phenylalanine amide.
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 14.3%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
Db 1 L 1

RESULT 13
PRCT CARMA STANDARD; PRT; 5 AA.
AC P67857; P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Proctolin.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=8623789; PubMed=2872661; DOI=10.1016/0196-9781(86)90063-X;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -!- FUNCTION: Stimulates cardiac output and hindgut motility,
CC modulates visceral and skeletal muscle in many arthropods.
CC -!- TISSUE SPECIFICITY: Secreted.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
KW Direct protein sequencing; Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 14.3%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
Db 3 L 3

RESULT 14
PRCT LIMPO STANDARD; PRT; 5 AA.
AC P67858; P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Proctolin.
OS Limulus polyphemus (Atlantic horseshoe crab).

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OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Meroostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_TaxID=6850;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90287800; PubMed=2356151; DOI=10.1016/0196-9781(90)90072-D;
RA Groomer J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
CC -!- FUNCTION: Stimulates cardiac output and hindgut motility,
CC modulates visceral and skeletal muscle in many arthropods.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Found in the crab pericardial organs.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A60411; A60411.
KW Direct protein sequencing; Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 14.3%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
Db 3 L 3

RESULT 15
PRCT PERAM STANDARD; PRT; 5 AA.
AC P67859; P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Blattellinae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=76074708; PubMed=576; DOI=10.1016/0024-3205(75)90134-4;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
CC -!- FUNCTION: Stimulates cardiac output and hindgut motility,
CC modulates visceral and skeletal muscle in many arthropods.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Found in the lateral white neurons.
CC -----
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CC removed.

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DR PIR; A01644; HOROHA.
KW Direct protein sequencing; Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;
Query Match 14.3%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 L 4
Db 3 L 3

Search completed: January 11, 2006, 15:34:04
Job time : 66 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:34:36 ; Search time 8 Seconds
(without alignments)
5.909 Million cell updates/sec

Title: US-10-786-774-16

Perfect score: 28

Sequence: 1 DKCLA 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 904

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_5/ptodata/2/pubpaa/US08_NEW_PUB_PEP.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_PEP.*
- 5: /cgn2_6/ptodata/2/pubpaa/US03_NEW_PUB_PEP.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_PEP.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB_PEP.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	64.3	5	6	US-10-997-081A-15
2	15	53.6	5	6	US-10-966-483-71
3	15	53.6	5	7	US-11-021-441-61
4	14	50.0	5	6	US-10-990-627-10
5	14	50.0	5	6	US-10-964-313-29
6	14	50.0	5	7	US-11-108-185-58
7	13	46.4	5	6	US-10-997-081A-12
8	13	46.4	5	6	US-10-997-081A-24
9	13	46.4	5	6	US-10-997-081A-33
10	11	39.3	5	6	US-10-977-367-10
11	11	39.3	5	6	US-10-977-367-12
12	11	39.3	5	6	US-10-977-367-39
13	11	39.3	5	6	US-10-484-271A-6
14	11	39.3	5	6	US-10-467-657-6740
15	11	39.3	5	6	US-10-636-320-9
16	11	39.3	5	6	US-10-636-320-10
17	11	39.3	5	6	US-10-997-081A-7
18	11	39.3	5	6	US-10-622-246-10
19	11	39.3	5	6	US-10-622-246-45
20	11	39.3	5	6	US-10-622-246-105
21	11	39.3	5	6	US-10-622-246-107
22	11	39.3	5	7	US-11-075-351-4
23	11	39.3	5	7	US-11-126-468-8
24	11	39.3	5	7	US-11-166-099-12
25	11	39.3	5	7	US-11-166-099-13

26	11	39.3	5	7	US-11-166-099-22
27	11	39.3	5	7	US-11-062-186-35
28	11	39.3	5	7	US-11-148-074-7
29	11	39.3	5	7	US-11-122-795-4
30	11	39.3	5	7	US-11-145-035-27
31	11	39.3	5	7	US-11-220-439-5
32	11	39.3	5	7	US-11-220-439-29
33	11	39.3	5	7	US-11-221-210-5
34	10	35.7	5	6	US-10-964-313-27
35	10	35.7	5	6	US-10-964-313-28
36	10	35.7	5	7	US-11-108-185-60
37	10	35.7	5	7	US-11-191-574-15
38	9	32.1	5	6	US-10-845-413-134
39	9	32.1	5	6	US-10-845-413-401
40	9	32.1	5	6	US-10-977-367-28
41	9	32.1	5	6	US-10-816-768-82
42	9	32.1	5	6	US-10-467-657-8919
43	9	32.1	5	6	US-10-849-107-6
44	9	32.1	5	6	US-10-763-712A-145
45	9	32.1	5	6	US-10-650-326B-26

ALIGNMENTS

RESULT 1

US-10-997-081A-15
; Sequence 15, Application US/10997081A
; Publication No. US20050287632A1
; GENERAL INFORMATION:
; APPLICANT: Holmquist, Barton
; APPLICANT: Strydom, Daniel
; APPLICANT: Restoragen Inc.
; TITLE OF INVENTION: Peptide Amidation Process
; FILE REFERENCE: 1627.012US1
; CURRENT APPLICATION NUMBER: US/10/997,081A
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: US 60/383,362
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic C-terminal sequence
US-10-997-081A-15

Query Match 64.3%; Score 18; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KCL 4

Db 2 KCL 4

RESULT 2

US-10-966-483-71
; Sequence 71, Application US/10966483
; Publication No. US20050281783A1
; GENERAL INFORMATION:
; APPLICANT: Kinch, Michael S.
; APPLICANT: Kienler, Peter A.
; APPLICANT: Bruckheimer, Elizabeth
; APPLICANT: Dubensky, Jr. Thomas W.
; APPLICANT: Cook, David N.
; TITLE OF INVENTION: LISTERIA-BASED EPHA2 VACCINES
; FILE REFERENCE: 10271-146
; CURRENT APPLICATION NUMBER: US/10/966,483
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/511,919

; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 60/511,719
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 60/532,666
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/556,631
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 2004-10-07
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-966-483-71

Query Match 53.6%; Score 15; DB 6; Length 5;
Best Local Similarity 75.0%; Pred. No. 5.2e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;
QY 1 DKCL 4
DB 1 DKAL 4

RESULT 3
US-11-021-441-61
; Sequence 61, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKI, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-021-441-61

Query Match 53.6%; Score 15; DB 7; Length 5;
Best Local Similarity 75.0%; Pred. No. 5.2e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;
QY 1 DKCL 4
DB 1 DKAL 4

RESULT 4

US-10-990-627-10
; Sequence 10, Application US/10990627
; Publication No. US20050255577A1
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Eric T
; TITLE OF INVENTION: CRYSTALLIZATION AND STRUCTURE OF STAPHYLOCOCCUS AUREUS PEPTIDE
; FILE REFERENCE: 268 63170102
; CURRENT APPLICATION NUMBER: US/10/990,627
; CURRENT FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: 09/896,580
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,550
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/215,555
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Amino Acid Residue
US-10-990-627-10

Query Match 50.0%; Score 14; DB 6; Length 5;
Best Local Similarity 66.7%; Pred. No. 5.2e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0;
Gaps 0;

QY 3 CLA 5
DB 3 CLS 5

RESULT 5
US-10-964-313-29
; Sequence 29, Application US/10964313
; Publication No. US20050287629A1
; GENERAL INFORMATION:
; APPLICANT: GROZINGER, CHRISTINA M.
; APPLICANT: HASSIG, CHRISTIAN A.
; APPLICANT: SCHREIBER, STUART L.
; TITLE OF INVENTION: CLASS II HUMAN HISTONE DEACETYLASES, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: H0V-037.02
; CURRENT APPLICATION NUMBER: US/10/964,313
; CURRENT FILING DATE: 2004-10-13
; PRIOR APPLICATION NUMBER: 09/800,187
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,802
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 29
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-964-313-29

Query Match 50.0%; Score 14; DB 6; Length 5;
Best Local Similarity 66.7%; Pred. No. 5.2e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;
QY 1 DKC 3
DB 2 DDC 4

RESULT 6
US-11-108-185-58
; Sequence 58, Application US/11108185
; Publication No. US20050262591A1

; GENERAL INFORMATION:
 ; APPLICANT: DeBonte, Lorin R.
 ; APPLICANT: Fan, Zhegong
 ; APPLICANT: Miao, Guo-Hua
 ; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
 ; FILE REFERENCE: 07148-063003
 ; CURRENT APPLICATION NUMBER: US/11/108,185
 ; CURRENT FILING DATE: 2005-04-18
 ; PRIOR APPLICATION NUMBER: US/09/771,904
 ; PRIOR FILING DATE: 2001-01-29
 ; PRIOR APPLICATION NUMBER: US 08/874,109
 ; PRIOR FILING DATE: 1997-06-12
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 58
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: exemplary motif
 US-11-108-185-58

Query Match 50.0%; Score 14; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KC 3
 Db 2 KC 3

RESULT 7
 US-10-997-081A-12
 ; Sequence 12, Application US/10997081A
 ; Publication No. US20050287632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Holmquist, Barton
 ; APPLICANT: Strydom, Daniel
 ; APPLICANT: Restoragen Inc.
 ; TITLE OF INVENTION: Peptide Amidation Process
 ; FILE REFERENCE: 1627.012US1
 ; CURRENT APPLICATION NUMBER: US/10/997,081A
 ; CURRENT FILING DATE: 2004-11-24
 ; PRIOR APPLICATION NUMBER: US 60/383,362
 ; PRIOR FILING DATE: 2002-05-24
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: A synthetic c-terminal sequence
 US-10-997-081A-12

Query Match 46.4%; Score 13; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CL 4
 Db 3 CL 4

RESULT 8
 US-10-997-081A-24
 ; Sequence 24, Application US/10997081A
 ; Publication No. US20050287632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Holmquist, Barton
 ; APPLICANT: Strydom, Daniel
 ; APPLICANT: Restoragen Inc.
 ; TITLE OF INVENTION: Peptide Amidation Process

; FILE REFERENCE: 1627.012US1
 ; CURRENT APPLICATION NUMBER: US/10/997,081A
 ; CURRENT FILING DATE: 2004-11-24
 ; PRIOR APPLICATION NUMBER: US 60/383,362
 ; PRIOR FILING DATE: 2002-05-24
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 24
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: A synthetic peptide
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: 1
 ; OTHER INFORMATION: Ala is a dehydroalanyl
 US-10-997-081A-24

Query Match 46.4%; Score 13; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CL 4
 Db 3 CL 4

RESULT 9
 US-10-997-081A-33
 ; Sequence 33, Application US/10997081A
 ; Publication No. US20050287632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Holmquist, Barton
 ; APPLICANT: Strydom, Daniel
 ; APPLICANT: Restoragen Inc.
 ; TITLE OF INVENTION: Peptide Amidation Process
 ; FILE REFERENCE: 1627.012US1
 ; CURRENT APPLICATION NUMBER: US/10/997,081A
 ; CURRENT FILING DATE: 2004-11-24
 ; PRIOR APPLICATION NUMBER: US 60/383,362
 ; PRIOR FILING DATE: 2002-05-24
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 33
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: A synthetic peptide
 US-10-997-081A-33

Query Match 46.4%; Score 13; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CL 4
 Db 1 CL 2

RESULT 10
 US-10-977-367-10
 ; Sequence 10, Application US/10977367
 ; Publication No. US20050245445A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hanahan, Douglas
 ; APPLICANT: Ruoslahti, Erkki
 ; TITLE OF INVENTION: Molecules That Selectively Home To
 ; TITLE OF INVENTION: Vasculature of Premalignant or Malignant Lesions of the
 ; TITLE OF INVENTION: Pancreas and Other Organs
 ; FILE REFERENCE: 66821-310
 ; CURRENT APPLICATION NUMBER: US/10/977,367

; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/516,118
; PRIOR FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Any Basic Amino Acid
US-10-977-367-10

Query Match 39.3%; Score 11; DB 6; Length 5;
Best Local Similarity 66.7%; Pred. No. 5.2e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CLA 5
| |
Db 1 CKA 3

RESULT 11
US-10-977-367-12
; Sequence 12, Application US/10977367
; Publication No. US20050245445A1
; GENERAL INFORMATION:
; APPLICANT: Hanahan, Douglas
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules That Selectively Home To
; TITLE OF INVENTION: Vasculature of Premalignant or Malignant Lesions of the
; TITLE OF INVENTION: Pancreas and Other Organs
; FILE REFERENCE: 66821-310
; CURRENT APPLICATION NUMBER: US/10/977,367
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/516,118
; PRIOR FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-977-367-12

Query Match 39.3%; Score 11; DB 6; Length 5;
Best Local Similarity 66.7%; Pred. No. 5.2e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CLA 5
| |
Db 1 CKA 3

RESULT 12
US-10-977-367-39
; Sequence 39, Application US/10977367
; Publication No. US20050245445A1
; GENERAL INFORMATION:
; APPLICANT: Hanahan, Douglas
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules That Selectively Home To
; TITLE OF INVENTION: Vasculature of Premalignant or Malignant Lesions of the
; TITLE OF INVENTION: Pancreas and Other Organs
; FILE REFERENCE: 66821-310
; CURRENT APPLICATION NUMBER: US/10/977,367
; CURRENT FILING DATE: 2004-10-29

; PRIOR APPLICATION NUMBER: 60/516,118
; PRIOR FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-977-367-39

Query Match 39.3%; Score 11; DB 6; Length 5;
Best Local Similarity 66.7%; Pred. No. 5.2e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CLA 5
| |
Db 1 CKA 3

RESULT 13
US-10-484-271A-6
; Sequence 6, Application US/10484271A
; Publication No. US20050255464A1
; GENERAL INFORMATION:
; APPLICANT: Hagen, Frederick S.
; APPLICANT: Woodbury, Richard G.
; APPLICANT: Oort, Pieter J.
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF PEPTIDYL COMPOUNDS
; TITLE OF INVENTION: INTERACTING WITH EXTRACELLULAR TARGET MOLECULES
; FILE REFERENCE: 17881-7-1US
; CURRENT APPLICATION NUMBER: US/10/484,271A
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/306,924
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/US02/23375
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enterokinase
; OTHER INFORMATION: recognition sequence
US-10-484-271A-6

Query Match 39.3%; Score 11; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2
| |
Db 4 DK 5

RESULT 14
US-10-467-657-6740
; Sequence 6740, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:29:54 ; Search time 22 Seconds
(without alignments)
18.790 Million cell updates/sec

Title: US-10-786-774-16

Perfect score: 28

Sequence: 1 DKCLA 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 17018

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 2: /cgm2_6/ptodata/1/iaa/6 COMB.pap.*
- 3: /cgm2_6/ptodata/1/iaa/H COMB.pap.*
- 4: /cgm2_6/ptodata/1/iaa/PCUTUS COMB.pap.*
- 5: /cgm2_6/ptodata/1/iaa/RE COMB.pap.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	71.4	5	2	US-09-187-859-669
2	20	71.4	5	2	US-09-305-927-79
3	20	71.4	5	2	US-09-073-040-7
4	20	71.4	5	2	US-09-375-808-29
5	20	71.4	5	2	US-09-839-542B-669
6	20	71.4	5	2	US-09-264-516A-79
7	20	71.4	5	2	US-09-234-395-55
8	20	71.4	5	2	US-09-305-928-55
9	20	71.4	5	2	US-10-006-869-669
10	18	64.3	5	2	US-09-001-984C-79
11	18	64.3	5	2	US-09-396-347F-79
12	17	60.7	5	2	US-09-375-808-33
13	16	57.1	5	1	US-08-976-703-2
14	16	57.1	5	2	US-09-187-859-3648
15	16	57.1	5	2	US-09-187-859-3663
16	16	57.1	5	2	US-09-375-808-22
17	16	57.1	5	2	US-09-375-808-23
18	16	57.1	5	2	US-09-839-542B-3648
19	16	57.1	5	2	US-09-839-542B-3663
20	16	57.1	5	2	US-09-788-006-2
21	16	57.1	5	2	US-09-788-006-3
22	16	57.1	5	2	US-10-006-869-3648
23	16	57.1	5	2	US-10-006-869-3663
24	15	53.6	5	1	US-07-671-757-6
25	15	53.6	5	1	US-08-199-778-5
26	15	53.6	5	1	US-08-098-313-4
27	15	53.6	5	2	US-09-187-859-2629

28 15 53.6 5 2 US-09-375-808-32 Sequence 32, Appl
29 15 53.6 5 2 US-09-375-808-34 Sequence 34, Appl
30 15 53.6 5 2 US-09-839-542B-2629 Sequence 2629, Ap
31 15 53.6 5 2 US-09-945-249-83 Sequence 83, Appl
32 15 53.6 5 2 US-09-041-990-83 Sequence 83, Appl
33 15 53.6 5 2 US-10-006-869-2629 Sequence 2629, Ap
34 15 53.6 5 4 PCT-US92-01188-4 Sequence 4, Appli
35 14 50.0 5 1 US-07-671-757-21 Sequence 21, Appl
36 14 50.0 5 1 US-07-671-757-22 Sequence 22, Appl
37 14 50.0 5 1 US-08-234-602-8 Sequence 8, Appli
38 14 50.0 5 1 US-08-363-475-13 Sequence 13, Appl
39 14 50.0 5 1 US-08-497-134A-30 Sequence 30, Appl
40 14 50.0 5 1 US-08-483-077C-1 Sequence 1, Appli
41 14 50.0 5 1 US-08-244-496-48 Sequence 48, Appl
42 14 50.0 5 1 US-08-244-496-52 Sequence 52, Appl
43 14 50.0 5 1 US-08-244-496-85 Sequence 85, Appl
44 14 50.0 5 1 US-08-531-525-2 Sequence 2, Appli
45 14 50.0 5 1 US-08-519-109B-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-187-859-669
; Sequence 669, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187.859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 669
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence
US-09-187-859-669

Query Match 71.4% Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
|||
Db 3 DKC 5

RESULT 2
US-09-305-927-79
; Sequence 79, Application US/09305927
; Patent No. 6433149
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING
; FILE REFERENCE: 100086.407C5
; CURRENT APPLICATION NUMBER: US/09/305.927
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 5
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin
; OTHER INFORMATION: cell adhesion recognition sequence
US-09-305-927-79

Query Match          71.4%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DKC 3
        |||
Db      3 DKC 5

RESULT 3
US-09-073-040-7
; Sequence 7, Application US/09073040
; Patent No. 6472367
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: OB-CADHERIN MEDIATED CELL ADHESION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/073,040
; APPLICATION NUMBER: US/09/073,040
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 100086.407
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
US-09-073-040-7

Query Match          71.4%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DKC 3
        |||
Db      3 DKC 5

RESULT 4
US-09-375-808-29
; Sequence 29, Application US/09375808
; Patent No. 6544750
; GENERAL INFORMATION:
; APPLICANT: Schmaier, Alvin H.
; APPLICANT: Hasan, Ahmed A.K.
; TITLE OF INVENTION: PEPTIDE ANALOGS AS SELECTIVE INHIBITORS OF THROMBIN
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; TITLE OF INVENTION: ACTIVATION OF PROTEASE ACTIVATED RECEPTOR 1
; FILE REFERENCE: 32921-149520
; CURRENT APPLICATION NUMBER: US/09/375,808
; CURRENT FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-375-808-29

Query Match          71.4%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DKC 3
        |||
Db      3 DKC 5

RESULT 5
US-09-839-542B-669
; Sequence 669, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 669
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence
US-09-839-542B-669

Query Match          71.4%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DKC 3
        |||
Db      3 DKC 5

RESULT 6
US-09-264-516A-79
; Sequence 79, Application US/09264516A
; Patent No. 6593297
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING
; TITLE OF INVENTION: CANCER METASTASIS
; FILE REFERENCE: 100086.407C3
; CURRENT APPLICATION NUMBER: US/09/264,516A
; CURRENT FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/234,395
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 09/187,859
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; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/073,040
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin
; OTHER INFORMATION: cell adhesion recognition sequence
US-09-264-516A-79

Query Match          71.4%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
Db 3 DKC 5

RESULT 7
US-09-234-395-55
; Sequence 55, Application US/09234395
; Patent No. 6680175
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C2
; CURRENT APPLICATION NUMBER: US/09/234,395
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; FEATURE:
; OTHER INFORMATION: OB-Cadherin
; OTHER INFORMATION: Cyclic Peptide
US-09-234-395-55

Query Match          71.4%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
Db 3 DKC 5

RESULT 8
US-09-305-928-55
; Sequence 55, Application US/09305928
; Patent No. 6682901
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C4
; CURRENT APPLICATION NUMBER: US/09/305,928
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
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; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: OB-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-305-928-55

Query Match          71.4%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
Db 3 DKC 5

RESULT 9
US-10-006-869-669
; Sequence 669, Application US/10006869
; Patent No. 6962969
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 669
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence
US-10-006-869-669

Query Match          71.4%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
Db 3 DKC 5

RESULT 10
US-09-001-984C-79
; Sequence 79, Application US/09001984C
; Patent No. 6245331
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Bellisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: NYU-011
; CURRENT APPLICATION NUMBER: US/09/001,984C
; CURRENT FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: 60/034,003
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
```

US-09-001-984C-79

Query Match 64.3%; Score 18; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.6e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKCL 4
|:|
Db 1 DECI 4

RESULT 11

US-09-396-347F-79
; Sequence 79, Application US/09396347F
; Patent No. 6506384
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: 32004-169276
; CURRENT APPLICATION NUMBER: US/09/396,347F
; CURRENT FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: 09/001,984
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-396-347F-79

Query Match 64.3%; Score 18; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.6e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKCL 4
|:|
Db 1 DECI 4

RESULT 12

US-09-375-808-33
; Sequence 33, Application US/09375808
; Patent No. 6544750
; GENERAL INFORMATION:
; APPLICANT: Schmaier, Alvin H.
; APPLICANT: Hasan, Ahmed A.K.
; TITLE OF INVENTION: PEPTIDE ANALOGS AS SELECTIVE INHIBITORS OF THROMBIN
; TITLE OF INVENTION: ACTIVATION OF PROTEASE ACTIVATED RECEPTOR 1
; FILE REFERENCE: 32921-149520
; CURRENT APPLICATION NUMBER: US/09/375,808
; CURRENT FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-375-808-33

Query Match 60.7%; Score 17; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
|:|
Db 3 DRC 5

RESULT 13

US-08-976-703-2
; Sequence 2, Application US/08976703
; Patent No. 5945288
; GENERAL INFORMATION:
; APPLICANT: CHANG, ZHIYUH
; APPLICANT: MORGAN, RICHARD D.
; TITLE OF INVENTION: METHOD FOR CLONING AND
; TITLE OF INVENTION: PRODUCING THE PmeI RESTRICTION ENDONUCLEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: New England Biolabs, Inc.
; STREET: 32 Tozer Road
; CITY: Beverly
; STATE: MA
; COUNTRY: US
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,703
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 978-927-5054
; TELEFAX: 978-927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-976-703-2

Query Match 57.1%; Score 16; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
|:|
Db 3 DEC 5

RESULT 14

US-09-187-859-3648
; Sequence 3648, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3648
; LENGTH: 5
; TYPE: PRT


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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-187-859-3648

Query Match          57.1%; Score 16; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DKC 3
       :||
Db      3 EKC 5

RESULT 15
US-09-187-859-3663
; Sequence 3663, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187.859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3663
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-187-859-3663

Query Match          57.1%; Score 16; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DKC 3
       :||
Db      3 EKC 5

Search completed: January 11, 2006, 15:35:04
Job time : 23 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:34:11 ; Search time 58 Seconds
(without alignments)
36.020 Million cell updates/sec

Title: US-10-786-774-16

Perfect score: 28

Sequence: 1 DKCLA 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 17739

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.*

- 1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	5	4	US-10-161-959-16
2	28	100.0	5	5	US-10-786-774-16
3	28	100.0	5	5	US-10-845-407-16
4	22	78.6	5	4	US-10-161-959-12
5	22	78.6	5	5	US-10-786-774-12
6	22	78.6	5	5	US-10-845-407-12
7	21	75.0	5	4	US-10-436-549-450
8	21	75.0	5	4	US-10-712-425-450
9	21	75.0	5	5	US-10-773-032-450
10	20	71.4	5	3	US-09-234-395-55
11	20	71.4	5	3	US-09-305-928-55
12	20	71.4	5	3	US-09-264-516A-79
13	20	71.4	5	4	US-10-006-869-669
14	20	71.4	5	4	US-10-141-357-79
15	20	71.4	5	4	US-10-395-032-669
16	20	71.4	5	5	US-10-759-379-55
17	20	71.4	5	5	US-10-759-507-55
18	20	71.4	5	5	US-10-808-187-1390
19	20	71.4	5	5	US-10-807-807-1390
20	20	71.4	5	6	US-11-004-107-669
21	20	71.4	5	6	US-11-003-150-57
22	18	64.3	5	4	US-10-161-959-15
23	18	64.3	5	5	US-10-786-774-15
24	18	64.3	5	5	US-10-845-407-15
25	17	60.7	5	4	US-10-206-699-32
26	17	60.7	5	4	US-10-436-549-281
27	17	60.7	5	4	US-10-436-549-459

28	17	60.7	5	4	US-10-712-425-281	Sequence 281, App
29	17	60.7	5	4	US-10-712-425-459	Sequence 459, App
30	17	60.7	5	5	US-10-773-032-281	Sequence 281, App
31	17	60.7	5	5	US-10-773-032-459	Sequence 459, App
32	16	57.1	5	3	US-09-788-006-2	Sequence 2, Appli
33	16	57.1	5	3	US-09-788-006-3	Sequence 3, Appli
34	16	57.1	5	4	US-10-006-869-3648	Sequence 3648, Ap
35	16	57.1	5	4	US-10-006-869-3663	Sequence 3663, Ap
36	16	57.1	5	4	US-10-395-032-3668	Sequence 3648, Ap
37	16	57.1	5	4	US-10-395-032-3663	Sequence 3663, Ap
38	16	57.1	5	4	US-10-237-673-2	Sequence 2, Appli
39	16	57.1	5	5	US-10-487-337-45	Sequence 45, Appli
40	16	57.1	5	5	US-11-004-107-3648	Sequence 3648, Ap
41	16	57.1	5	6	US-11-004-107-3663	Sequence 3663, Ap
42	15	53.6	5	3	US-09-945-249-83	Sequence 83, Appli
43	15	53.6	5	4	US-10-006-869-2629	Sequence 2629, Ap
44	15	53.6	5	4	US-10-262-832-3	Sequence 3, Appli
45	15	53.6	5	4	US-10-283-940-48	Sequence 48, Appli

ALIGNMENTS

RESULT 1

US-10-161-959-16

; Sequence 16, Application US/10161959

; Publication No. US20030096748A1

; GENERAL INFORMATION:

; APPLICANT: Holoshitz, Joseph

; APPLICANT: Ling, Song

; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases Associated

; FILE OF INVENTION: Signal Transduction Aberrations

; CURRENT APPLICATION NUMBER: US/10/161,959

; CURRENT FILING DATE: 2002-10-01

; PRIOR APPLICATION NUMBER: 60/295,691

; PRIOR FILING DATE: 2001-06-04

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 16

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

; US-10-161-959-16

Query Match 100.0%; Score 28; DB 4; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKCLA 5

DB 1 DKCLA 5

RESULT 2

US-10-786-774-16

; Sequence 16, Application US/10786774

; Publication No. US20040236071A1

; GENERAL INFORMATION:

; APPLICANT: Holoshitz, Joseph

; APPLICANT: Ling, Song

; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases Associated

; FILE OF INVENTION: with Signal Transduction Aberrations

; FILE REFERENCE: UM-08550

; CURRENT APPLICATION NUMBER: US/10/786,774

; CURRENT FILING DATE: 2004-02-25

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 16

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-786-774-16

Query Match 100.0%; Score 28; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKCLA 5
Db 1 DKCLA 5

RESULT 3

US-10-845-407-16
; Sequence 16, Application US/10845407
; Publication No. US20050013820A1
; GENERAL INFORMATION:
; APPLICANT: Holoshitz, Joseph
; APPLICANT: Ling, Song
; TITLE OF INVENTION: Methods and Compositions for the Treatment of MHC-Associated
; FILE REFERENCE: UM-08912
; CURRENT APPLICATION NUMBER: US/10/845,407
; CURRENT FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-845-407-16

Query Match 100.0%; Score 28; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKCLA 5
Db 1 DKCLA 5

RESULT 4

US-10-161-959-12
; Sequence 12, Application US/10161959
; Publication No. US20030096748A1
; GENERAL INFORMATION:
; APPLICANT: Holoshitz, Joseph
; APPLICANT: Ling, Song
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases Associated
; FILE REFERENCE: UM-07135
; CURRENT APPLICATION NUMBER: US/10/161,959
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,691
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-161-959-12

Query Match 78.6%; Score 22; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KCLA 5
Db 2 KCLA 5

RESULT 5
US-10-786-774-12
; Sequence 12, Application US/10786774
; Publication No. US20040236071A1
; GENERAL INFORMATION:
; APPLICANT: Holoshitz, Joseph
; APPLICANT: Ling, Song
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases Associated
; FILE REFERENCE: UM-08550
; CURRENT APPLICATION NUMBER: US/10/786,774
; CURRENT FILING DATE: 2004-02-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-786-774-12

Query Match 78.6%; Score 22; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KCLA 5
Db 2 KCLA 5

RESULT 6

US-10-845-407-12
; Sequence 12, Application US/10845407
; Publication No. US20050013820A1
; GENERAL INFORMATION:
; APPLICANT: Holoshitz, Joseph
; APPLICANT: Ling, Song
; TITLE OF INVENTION: Methods and Compositions for the Treatment of MHC-Associated
; FILE REFERENCE: UM-08912
; CURRENT APPLICATION NUMBER: US/10/845,407
; CURRENT FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-845-407-12

Query Match 78.6%; Score 22; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KCLA 5
Db 2 KCLA 5

RESULT 7

US-10-436-549-450
; Sequence 450, Application US/10436549
; Publication No. US20040038307A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank D.

APPLICANT: Meng, Dr. Xun
APPLICANT: Chan, John W.
APPLICANT: Zhang, Shengsheng
APPLICANT: Benkovic, Stephen J.
TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN
TITLE OF INVENTION: PROTEIN ANALYSIS
FILE REFERENCE: ENGE-P01-001
CURRENT APPLICATION NUMBER: US/10/436,549
CURRENT FILING DATE: 2003-05-12
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/393,233
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,235
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,211
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,280
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,197
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,223
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/430,948
PRIOR FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/433,319
PRIOR FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: 60/433,137
PRIOR FILING DATE: 2002-07-01
NUMBER OF SEQ ID NOS: 614
SOFTWARE: PatentIn version 3.2
SEQ ID NO 450
TYPE: PRT
ORGANISM: Human
US-10-436-549-450

Query Match 75.0%; Score 21; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKCL 4
|:|
Db 1 DRCL 4

RESULT 8
US-10-712-425-450
Sequence 450, Application US/10712425
Publication No. US20040180380A1
GENERAL INFORMATION:
APPLICANT: LEE, FRANK D.
APPLICANT: LIVINGSTON, DAVID
TITLE OF INVENTION: PROTEOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN
TITLE OF INVENTION: MODIFICATION ANALYSIS
FILE REFERENCE: ENGE-P02-001
CURRENT APPLICATION NUMBER: US/10/712,425
CURRENT FILING DATE: 2003-11-13
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/379,626
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,137
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,197
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,211
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,223
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,233
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,235
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,280
PRIOR FILING DATE: 2002-07-01
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn version 3.2
SEQ ID NO 450
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-10-773-032-450

Query Match 75.0%; Score 21; DB 5; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKCL 4
|:|
Db 1 DRCL 4

RESULT 9
US-10-773-032-450
Sequence 450, Application US/10773032
Publication No. US20050069911A1
GENERAL INFORMATION:
APPLICANT: LEE, FRANK D.
APPLICANT: MENG, XUN
APPLICANT: AFEYAN, NOUBAR B.
TITLE OF INVENTION: PROTEOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN
TITLE OF INVENTION: MODIFICATION ANALYSIS
FILE REFERENCE: ENGE-P03-001
CURRENT APPLICATION NUMBER: US/10/773,032
CURRENT FILING DATE: 2004-02-05
PRIOR FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: 10/712,425
PRIOR FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: 10/436,549
PRIOR FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/379,626
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/393,137
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,197
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,211
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,223
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,233
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,235
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/393,280
PRIOR FILING DATE: 2002-07-01
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn version 3.2
SEQ ID NO 450
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-10-773-032-450

Query Match 75.0%; Score 21; DB 5; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKCL 4
|:|
Db 1 DRCL 4

RESULT 10
US-09-234-395-55
; Sequence 55, Application US/09234395
; Patent No. US20020123044A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C2
; CURRENT APPLICATION NUMBER: US/09/234,395
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: OB-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-234-395-55

Query Match 71.4%; Score 20; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
|||
Db 3 DKC 5

RESULT 11
US-09-305-928-55
; Sequence 55, Application US/09305928
; Patent No. US20020146687A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C4
; CURRENT APPLICATION NUMBER: US/09/305,928
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: OB-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-305-928-55

Query Match 71.4%; Score 20; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
|||
Db 3 DKC 5

RESULT 12

US-09-264-516A-79
; Sequence 79, Application US/09264516A
; Patent No. US20020169106A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING
; TITLE OF INVENTION: CANCER METASTASIS
; FILE REFERENCE: 100086.407C3
; CURRENT APPLICATION NUMBER: US/09/264,516A
; CURRENT FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/234,395
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 09/187,859
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/073,040
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin
; OTHER INFORMATION: cell adhesion recognition sequence
US-09-264-516A-79

Query Match 71.4%; Score 20; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
|||
Db 3 DKC 5

RESULT 13
US-10-006-869-669
; Sequence 669, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 669
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence
US-10-006-869-669

Query Match 71.4%; Score 20; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
|||
Db 3 DKC 5

RESULT 14
US-10-141-357-79

; Sequence 79, Application US/10141357
; Publication No. US20030096746A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING
; TITLE OF INVENTION: CANCER METASTASIS
; FILE REFERENCE: 100086.407C8
; CURRENT APPLICATION NUMBER: US/10/141,357
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin
; OTHER INFORMATION: cell adhesion recognition sequence
US-10-141-357-79

Query Match 71.4%; Score 20; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
|||
Db 3 DKC 5

RESULT 15
US-10-395-032-669
; Sequence 669, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 669
; LENGTH: 5
; TYPE: *PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence
US-10-395-032-669

Query Match 71.4%; Score 20; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
|||
Db 3 DKC 5

Search completed: January 11, 2006, 15:43:45
Job time : 59 secs

This Data Bank is a

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:27:44 ; Search time 15 Seconds
(without alignments)
32.072 Million cell updates/sec

Title: US-10-786-774-16

Perfect score: 28

Sequence: 1 DKCLA 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 120

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	39.3	5	2	PT0689 photosystem I 10.4
2	11	39.3	5	2	PT0660 T-cell receptor be
3	10	35.7	5	2	B22565 R-phycoerythrin al
4	10	35.7	5	2	A33882 cadmium-binding pe
5	10	35.7	5	2	B45525 actin I - malaria
6	10	35.7	5	2	S65726 hemoglobin, extrac
7	9	32.1	5	2	F22565 R-phycoerythrin ga
8	8	28.6	5	2	S55237 zinc-binding prote
9	8	28.6	5	2	PT0513 T-cell receptor be
10	8	28.6	5	2	PT0672 T-cell receptor be
11	8	28.6	5	2	B44817 34.5K structural p
12	8	28.6	5	2	D44817 35K structural p
13	7	25.0	5	2	D60274 major protein anti
14	7	25.0	5	2	PT0281 Ig heavy chain CRD
15	7	25.0	5	2	PT0656 T-cell receptor be
16	7	25.0	5	2	PT0573 T-cell receptor be
17	7	25.0	5	2	S68326 blood cell protein
18	7	25.0	5	2	A32014 trAM protein - Esc
19	6	21.4	5	2	A32516 cholecystokinin-5
20	6	21.4	5	2	I40702 primase - Citrobac
21	6	21.4	5	2	B31836 20K protein - Rick
22	6	21.4	5	2	I39964 ribosomal protein
23	6	21.4	5	2	I39966 ribosomal protein
24	6	21.4	5	2	I39965 ribosomal protein
25	6	21.4	5	2	B60274 major protein anti
26	6	21.4	5	2	S70615 endo-1,4-beta-xyla
27	6	21.4	5	2	JH0253 gut pentapeptide -
28	6	21.4	5	2	PT0267 Ig heavy chain CRD
29	6	21.4	5	2	PT0308 Ig heavy chain CRD

30	6	21.4	5	2	B44823 synaptosomal-assoc
31	6	21.4	5	2	PT0596 T-cell receptor be
32	6	21.4	5	2	PT0729 T-cell receptor be
33	6	21.4	5	2	PT0624 T-cell receptor be
34	6	21.4	5	2	PT0651 T-cell receptor be
35	6	21.4	5	2	PT0535 T-cell receptor be
36	6	21.4	5	2	PT0699 T-cell receptor be
37	6	21.4	5	2	PT0561 T-cell receptor be
38	6	21.4	5	2	PT0703 T-cell receptor be
39	6	21.4	5	2	PT0690 T-cell receptor be
40	6	21.4	5	2	PT0580 T-cell receptor be
41	6	21.4	5	2	PT0679 T-cell receptor be
42	6	21.4	5	2	H44817 34.5K structural p
43	6	21.4	5	2	F44817 34.5K structural p
44	6	21.4	5	2	I40698 biotin B - Citroba
45	6	21.4	5	2	PT0600 T-cell receptor be

ALIGNMENTS

RESULT 1

PQ0689 photosystem I 10.4K H1 chain - common tobacco (fragment)

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999

C;Accession: PQ0689

R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.

Plant Physiol. 102, 1259-1267, 1993

A;Title: Molecular heterogeneity of photosystem I. psad, psae, psaf, psah and psal are a

A;Reference number: PQ0667; MUID:94105345; PMID:8278548

A;Accession: PQ0689

A;Molecule type: protein

A;Residues: 1-5 <OBO>

A;Cross-references: UNIPARC:UPI000017B0AA

C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 39.3%; Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2

Db 4 DK 5

RESULT 2

PT0660 T-cell receptor beta chain V-D-J region (121-1BL) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0660

R;Feeney, A.J

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0660

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FEE>

A;Cross-references: UNIPARC:UPI000017C7EB

A;Experimental source: day 4 postnatal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 39.3%; Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2

Db 4 DK 5

RESULT 3
B22565
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
C/Species: Gastroclonium coulteri
C/Date: 07-Mar-1998 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C/Accession: B22565
R/Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A/Title: Characterization of the Bilin attachment sites in R-phycoerythrin.
A/Reference number: A22565; MUID:85182601; PMID:3886644
A/Accession: B22565
A/Molecule type: protein
A/Residues: 1-5 <KLO>
A/Cross-references: UNIPARC:UPI000017AEC3

Query Match 35.7%; Score 10; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CL 4
|:
2 CV 3
Db

RESULT 4
A33882
cadmium-binding pentapeptide - downy thornapple
C/Species: Datura innoxia (downy thornapple)
C/Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C/Accession: A33882
R/Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A/Title: Poly(Gamma-glutamylcysteinylglycine: its role in cadmium resistance in plant
A/Reference number: A94182; MUID:88016144; PMID:3477793
A/Accession: A33882
A/Molecule type: protein
A/Residues: 1-5 <JAC>
A/Cross-references: UNIPARC:UPI000017B088

Query Match 35.7%; Score 10; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KC 3
|:
1 EC 2
Db

RESULT 5
B45525
actin I - malaria parasite (Plasmodium falciparum) (fragments)
C/Species: Plasmodium falciparum
C/Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C/Accession: B45525
R/Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmak
Mol. Biochem. Parasitol. 35, 167-176, 1989
A/Title: Stage-specific expression and genomic organization of the actin genes of the ma
A/Reference number: A45525; MUID:89364996; PMID:2671721
A/Accession: B45525
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-5 <WES>
A/Cross-references: UNIPARC:UPI000017B5EC; GB:J03988
A/Note: the authors translated the codon GAA for residue 3 as Gly
C/Comment: The actin I gene contains no introns.

Query Match 35.7%; Score 10; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KC 3
|:
3 EC 4
Db

RESULT 6
S65726
hemoglobin, extracellular, chain b - earthworm (Lumbricus terrestris) (fragment)
C/Species: Lumbricus terrestris (common earthworm)
C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C/Accession: S65726
R/Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A/Title: Characterization of the constituent polypeptides of the extracellular hemoglobi
A/Reference number: S65721; MUID:96176855; PMID:8597573
A/Accession: S65726
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-5 <FUS>
A/Cross-references: UNIPARC:UPI000017BD81

Query Match 35.7%; Score 10; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KC 3
|:
3 QC 4
Db

RESULT 7
F22565
R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)
C/Species: Gastroclonium coulteri
C/Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C/Accession: F22565
R/Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A/Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A/Reference number: A22565; MUID:85182601; PMID:3886644
A/Accession: F22565
A/Molecule type: protein
A/Residues: 1-5 <KLO>
A/Cross-references: UNIPARC:UPI000017AEC4

Query Match 32.1%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|:
3 C 3
Db

RESULT 8
S55237
zinc-binding protein ZBP14 - maize (fragment)
C/Species: Zea mays (maize)
C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C/Accession: S55237
R/Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.
Biochem. J. 307, 267-272, 1995
A/Title: Expression and characterization of maize ZBP14, a member of a new family of zin
A/Reference number: S55237; MUID:95234046; PMID:7717986
A/Accession: S55237
A/Molecule type: protein
A/Residues: 1-5 <ROB>
A/Cross-references: UNIPARC:UPI000014515E

Query Match 28.6%; Score 8; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LA 5
|:
1 LA 2
Db

RESULT 9

PT0513
T-cell receptor beta chain V-D-J region (100-4AL) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0513; PT0606
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0513
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE2>
A;Cross-references: UNIPARC:UPI000017C7BC
A;Experimental source: adult thymus, strain BALB/c, clone 100-4AL
A;Accession: PT0606
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE2>
A;Cross-references: UNIPARC:UPI000017C7BC
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1S
C;Keywords: T-cell receptor

Query Match 28.6%; Score 8; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2

Db 4 DR 5

RESULT 10

PT0672
T-cell receptor beta chain V-D-J region (121-1B) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0646; PT0672
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0646
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE2>
A;Cross-references: UNIPARC:UPI000017C7E9
A;Experimental source: day 4 postnatal thymus, strain BALB/c, clone 121-1B
A;Accession: PT0672
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Cross-references: UNIPARC:UPI000017C7E9
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 140-1BG
C;Keywords: T-cell receptor

Query Match 28.6%; Score 8; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2

Db 4 DR 5

RESULT 11

B44817
34.5K structural protein - Leuconostoc oenos phage PZt11-15 (fragment)
C;Species: Leuconostoc oenos phage PZt11-15
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998

C;Accession: B44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: B44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Cross-references: UNIPARC:UPI000017CA40
A;Note: sequence extracted from NCBI backbone (NCBIP:70342)

Query Match 28.6%; Score 8; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LA 5

Db 1 LA 2

RESULT 12

D44817
35K structural protein - Leuconostoc oenos phage PAT5-12 (fragment)
C;Species: Leuconostoc oenos phage PAT5-12
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: D44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: D44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Cross-references: UNIPARC:UPI000017CA40
A;Note: sequence extracted from NCBI backbone (NCBIP:70340)

Query Match 28.6%; Score 8; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LA 5

Db 1 LA 2

RESULT 13

D60274
major protein antigen MPT46 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: D60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the culture
A;Reference number: A60274; MUID:91099989; PMID:1898899
A;Accession: D60274
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>
A;Cross-references: UNIPARC:UPI0000150742

Query Match 25.0%; Score 7; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2

Db 4 EK 5

RESULT 14

PT0281
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0281
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0281
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Cross-references: UNIPARC:UPI000017C205
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 7; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2
|:
Db 1 DE 2

RESULT 15
PT0656
T-cell receptor beta chain V-D-J region (121-1J) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0656
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0656
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Cross-references: UNIPARC:UPI000017C7F0
A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 25.0%; Score 7; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2
|:
Db 4 DE 5

Search completed: January 11, 2006, 15:34:30
Job time : 15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:23:19 ; Search time 129 Seconds

(without alignments)
17.030 Million cell updates/sec

Title: US-10-786-774-16

Perfect score: 28

Sequence: 1 DKCLA 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 31664

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	5	6 AAG79805	Aag79805 SE motif
2	28	100.0	5	9 ADW70979	Adw70979 HLA-DRB1*
3	22	78.6	5	6 AAG79800	Aag79800 SE motif
4	22	78.6	5	9 ADW70975	Adw70975 Human Apo
5	21	75.0	5	5 AAM52880	Aam52880 Plasmodiu
6	21	75.0	5	5 AAM52881	Aam52881 Plasmodiu
7	21	75.0	5	8 ADM10126	Adm10126 Human pro
8	21	75.0	5	8 ADR71292	Adr71292 Human pro
9	21	75.0	5	5 ADY95629	Ady95629 Human pep
10	20	71.4	5	3 AAY73549	Aay73549 OB-cadher
11	20	71.4	5	3 AAY60635	Aay60635 OB-cadher
12	20	71.4	5	4 AAB72592	Aab72592 Thrombin-
13	20	71.4	5	5 AAM52879	Aam52879 Plasmodiu
14	20	71.4	5	5 ABG92247	Abg92247 OB-cadher
15	20	71.4	5	6 ABU55761	Abu55761 OB-cadher
16	20	71.4	5	6 ABU59970	Abu59970 OB-cadher
17	20	71.4	5	7 ADC27139	Adc27139 Cyclic OB
18	20	71.4	5	7 ADC68593	Adc68593 Thiol-con
19	20	71.4	5	7 ADC68596	Adc68596 Thiol-con
20	20	71.4	5	8 ADT40402	Adt40402 hSARS vir
21	20	71.4	5	8 ADS79819	Ads79819 SARS viru
22	20	71.4	5	8 ADT37932	Adt37932 hSARS vir
23	20	71.4	5	9 ADV77626	Adv77626 Human Ob-
24	18	64.3	5	2 AAW70182	Aaw70182 N-termina

25	18	64.3	5	4 AAE05638	Aae05638 N-termina
26	18	64.3	5	5 AAM52870	Aam52870 Plasmodiu
27	18	64.3	5	5 AAM52871	Aam52871 Plasmodiu
28	18	64.3	5	5 AAM52869	Aam52869 Plasmodiu
29	18	64.3	5	6 AAG79804	Aag79804 SE motif
30	18	64.3	5	6 ABO43502	Abc43502 M. tuberc
31	18	64.3	5	7 ADF12074	Adf12074 Mycobacte
32	18	64.3	5	8 ADG76281	Adg76281 C-termina
33	18	64.3	5	9 ADW70978	Adw70978 HLA-DRB1*
34	17	60.7	5	4 AAB72596	Aab72596 Thrombin-
35	17	60.7	5	4 AAB37557	Aab37557 CD8 activ
36	17	60.7	5	7 ADC17431	Adc17431 Type IV c
37	17	60.7	5	8 ADM09957	Adm09957 Human pro
38	17	60.7	5	8 ADM10135	Adm10135 Human pro
39	17	60.7	5	8 ADR18953	Adr18953 Human typ
40	17	60.7	5	8 ADR71301	Adr71301 Human pro
41	17	60.7	5	8 ADR71123	Adr71123 Human pro
42	17	60.7	5	9 ADY92801	Ady92801 Nanoparti
43	17	60.7	5	9 ADY95638	Ady95638 Human pep
44	17	60.7	5	9 ADY95460	Ady95460 Human pep
45	16	57.1	5	1 AAP83013	Aap83013 Factor IX

ALIGNMENTS

RESULT 1
AAG79805
ID AAG79805 standard; peptide; 5 AA.

XX AC AAG79805;

XX DT 16-APR-2003 (first entry)

XX DE SE motif based peptide #3.

KW Motif: SE; signal transduction; Alzheimer's disease; neuronal cell;
KW calcitriculin; arrhythmia; idiopathic nephritic syndrome;
KW non-autoimmune hyperthyroidism; obesity; polycystic kidney disease;
KW cancer; asthma; atopic dermatitis; psoriasis; rheumatoid arthritis;
KW systemic lupus erythematosus; infectious disease; atherosclerosis;
KW inflammatory bowel disease; osteoarthritis; septic shock;
KW congestive heart failure; insulin-resistance syndrome;
KW ischaemia-reperfusion injury.

XX OS Homo sapiens.

XX WO200299061-A2.

XX PD 12-DEC-2002.

XX PF 04-JUN-2002; 2002WO-US017536.

XX PR 04-JUN-2001; 2001US-0295691P.

XX PR 03-JUN-2002; 2002US-00161959.

XX (UNMI) UNIV MICHIGAN.

XX PI Holoshitz J, Ling S;

XX DR WPI; 2003-156853/15.

XX Treating diseases associated with signal transduction aberrations, e.g.
PT Alzheimer's disease, arrhythmia or rheumatoid arthritis, comprises
PT administering a preparation comprising an SE- or an SE motif-containing
PT peptide.

XX Example 4; Page 63; 97pp; English.

XX The sequences given in AAG79903-05 represent peptides which are based on
CC the shared epitope (SE)-motif. These peptides were tested in DNA repair
CC assays. Peptides containing the SE motifs may be used in the method of the
CC invention for treating diseases associated with signal transduction

CC aberrations. The method comprises: (a) providing a subject with one or
CC more symptoms of Alzheimer's disease and, optionally, a plurality of
CC neuronal cells expressing calreticulin, and a preparation comprising an
CC SE-containing peptide or a peptide which binds the calreticulin; and (b)
CC administering the preparation to the subject. The inventive method is
CC useful for treating diseases associated with signal transduction
CC aberrations, such as Alzheimer's disease, arrhythmia, idiopathic
CC nephritic syndrome, non-autoimmune hyperthyroidism, obesity, polycystic
CC kidney disease, cancer, asthma, atopic dermatitis, psoriasis, rheumatoid
CC arthritis, systemic lupus erythematosus, infectious diseases,
CC inflammatory bowel disease, osteoarthritis, septic shock,
CC atherosclerosis, congestive heart failure, insulin-resistance syndrome,
CC and ischaemia-reperfusion injury
XX
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 28; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKCLA 5
Db 1 DKCLA 5
|||||
1 DKCLA 5

RESULT 2
ADW70979
ID ADMW70979 standard; peptide; 5 AA.
XX
XX AC ADW70979;
XX
XX DT 07-APR-2005 (first entry)
XX
XX DE HLA-DRB1*0404 shared epitope motif-containing mutant peptide, SEQ ID 16.
XX
XX KW Therapy; immune modulation; pharmaceutical; inflammation;
XX anti-inflammatory; immune disorder; antiarthritic; osteopathic;
XX antirheumatic; rheumatoid arthritis; Alzheimer's disease;
XX human leukocyte antigen; hla; mutein; calreticulin antagonist.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX DN US2005013820-A1.
XX
XX PD 20-JAN-2005.
XX
XX PF 13-MAY-2004; 2004US-00845407.
XX
XX PR 03-JUN-2002; 2002US-00161959.
XX
XX PA (UNMI) UNIV MICHIGAN.
XX
XX PI Holoshitz J, Ling S;
XX
XX DR WPT; 2005-090627/10.
XX
XX DR Treating rheumatoid arthritis by administering preparation comprising
XX shared epitope antagonist-containing peptide, to subject under suitable
XX conditions for improving symptoms involved in disease.
XX
XX PS Claim 3; SEQ ID NO 16; 84pp; English.
XX
XX CC The present invention relates to a method of treating rheumatoid
XX arthritis. The method involves providing a subject with one or more signs
XX or symptoms of rheumatoid arthritis and a preparation comprising a shared
XX epitope antagonist-containing peptide and administering the preparation
XX to the subject under conditions such that one or more signs or symptoms
XX are improved. The invention is useful for treating rheumatoid arthritis
XX and Alzheimer's disease. The present sequence is the human leukocyte
XX antigen (HLA)-DRB1 DRbeta*0404 chain shared epitope (SE) motif-containing
XX mutant peptide.

SQ Sequence 5 AA;

Query Match 100.0%; Score 28; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKCLA 5
Db 1 DKCLA 5
|||||
1 DKCLA 5

RESULT 3
AAG79800
ID AAG79800 standard; peptide; 5 AA.
XX
XX AC AAG79800;
XX
XX DT 16-APR-2003 (first entry)
XX
XX DE SE motif #5.
XX
XX KW Motif; SE; signal transduction; Alzheimer's disease; neuronal cell;
XX calreticulin; arrhythmia; idiopathic nephritic syndrome;
XX non-autoimmune hyperthyroidism; obesity; polycystic kidney disease;
XX cancer; asthma; atopic dermatitis; psoriasis; rheumatoid arthritis;
XX systemic lupus erythematosus; infectious disease; atherosclerosis;
XX inflammatory bowel disease; osteoarthritis; septic shock;
XX congestive heart failure; insulin-resistance syndrome;
XX ischaemia-reperfusion injury.
XX
XX OS Homo sapiens.
XX
XX PN WC200299061-A2.
XX
XX PD 12-DEC-2002.
XX
XX PF 04-JUN-2002; 2002WO-US017536.
XX
XX PR 04-JUN-2001; 2001US-0295691P.
XX
XX PR 03-JUN-2002; 2002US-00161959.
XX
XX PA (UNMI) UNIV MICHIGAN.
XX
XX PI Holoshitz J, Ling S;
XX
XX DR WPT; 2003-156853/15.
XX
XX PT Treating diseases associated with signal transduction aberrations, e.g.
XX Alzheimer's disease, arrhythmia or rheumatoid arthritis, comprises
XX administering a preparation comprising an SE- or an SE motif-containing
XX peptide.
XX
XX PS Claim 15; Page 34; 97pp; English.
XX
XX CC The sequences given in AAG79799-801 represent peptide motifs which are
XX contained in shared epitope (SE)-containing peptides. Peptides containing
XX these motifs may be used in the method of the invention for treating
XX diseases associated with signal transduction aberrations. The method
XX comprises: (a) providing a subject with one or more symptoms of
XX Alzheimer's disease and, optionally, a plurality of neuronal cells
XX expressing calreticulin, and a preparation comprising an SE-containing
XX peptide or a peptide which binds the calreticulin; and (b) administering
XX the preparation to the subject. The inventive method is useful for
XX treating diseases associated with signal transduction aberrations, such
XX as Alzheimer's disease, arrhythmia, idiopathic nephritic syndrome, non-
XX autoimmune hyperthyroidism, obesity, polycystic kidney disease, cancer,
XX asthma, atopic dermatitis, psoriasis, rheumatoid arthritis, systemic
XX lupus erythematosus, infectious diseases, inflammatory bowel disease,
XX osteoarthritis, septic shock, atherosclerosis, congestive heart failure,
XX insulin-resistance syndrome, and ischaemia-reperfusion injury
XX
XX PS Sequence 5 AA;

Query Match 78.6%; Score 22; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KCLA 5
 Db 2 KCLA 5

RESULT 4
 ADW70975
 ID ADW70975 standard; peptide; 5 AA.
 XX
 AC ADW70975;
 XX
 XX 07-APR-2005 (first entry)
 XX
 XX Human ApoE2/ApoE4-derived peptide, SEQ ID 12.
 XX
 XX Therapy; immune modulation; pharmaceutical; inflammation;
 KW antinflammatory; immune disorder; antiarthritic; osteopathic;
 KW antirheumatic; rheumatoid arthritis; Alzheimer's disease;
 KW apolipoprotein e.
 XX
 XX Homo sapiens.
 OS
 XX US2005013820-A1.
 PN
 XX 20-JAN-2005.
 PD
 XX 13-MAY-2004; 2004US-00845407.
 PP
 XX 03-JUN-2002; 2002US-00161959.
 PR
 XX (UNMI) UNIV MICHIGAN.
 PA
 XX Holoshitz J, Ling S;
 PI
 XX WPI; 2005-090627/10.
 DR
 XX
 XX Treating rheumatoid arthritis by administering preparation comprising
 PT shared epitope antagonist-containing peptide, to subject under suitable
 PT conditions for improving symptoms involved in disease.
 XX
 XX Example 4; SEQ ID NO 12; 84pp; English.
 PS
 XX The present invention relates to a method of treating rheumatoid
 CC arthritis. The method involves providing a subject with one or more signs
 CC or symptoms of rheumatoid arthritis and a preparation comprising a shared
 CC epitope antagonist-containing peptide and administering the preparation
 CC to the subject under conditions such that one or more signs or symptoms
 CC are improved. The invention is useful for treating rheumatoid arthritis
 CC and Alzheimer's disease. The present sequence is the human apolipoprotein
 CC e (ApoE2/ApoE4)-derived peptide.
 XX
 XX Sequence 5 AA;
 SQ

Query Match 78.6%; Score 22; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KCLA 5
 Db 2 KCLA 5

RESULT 5
 AAM52880
 ID AAM52880 standard; peptide; 5 AA.
 XX
 AC AAM52880;
 XX
 XX 22-FEB-2002 (first entry)
 DT

Query Match 75.0%; Score 21; DB 5; Length 5;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKCL 4
 Db 2 DKCV 5

RESULT 6
 AAM52881
 ID AAM52881 standard; peptide; 5 AA.
 XX
 AC AAM52881;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX Plasmodium falciparum MSP1-19 peptide #39, used in epitope mapping.
 DE
 XX

XX Plasmodium falciparum MSP1-19 peptide #38, used in epitope mapping.
 DE
 XX Merozoite surface protein 1; MSP1-19; C-terminal region; epitope mapping;
 KW immunological assay; epitope expression; disease diagnosis;
 KW therapeutic target identification; drug discovery; development;
 KW binding activity determination; pharmacoproteomics;
 KW agricultural biotechnology; structural bioinformatics.
 XX
 OS Plasmodium falciparum.
 PN WO200188538-A2.
 XX
 PD 22-NOV-2001.
 XX
 XX 10-MAY-2001; 2001WO-US015450.
 PF
 XX 12-MAY-2000; 2000US-00569713.
 PR
 XX (DUMA/) DUMAS D P.
 PA
 XX Dumas DP;
 PI
 XX WPI; 2002-049548/06.
 DR
 XX A composition comprising reagent ligands attached to a solid support and
 PT reagent antibodies specifically bound to the ligands, useful in drug
 PT development, diagnostics and immunological assays for determining epitope
 PT expression.
 XX
 XX Example 1; Page 41; 55pp; English.
 PS
 XX The invention relates to compositions and methods for epitope mapping.
 CC The invention encompasses a composition comprising a diverse population
 CC of reagent ligands attached to a solid support and a diverse population
 CC of reagent-specific antibodies specifically bound to the ligands. The
 CC invention also encompasses a method for the determination of an epitope
 CC in a sample using the composition, and methods for diagnosing a disease,
 CC identifying a potential therapeutic target, mapping accessible epitopes
 CC of a polypeptide, and determining a binding activity in a sample. The
 CC composition of the invention may therefore be used in drug target
 CC discovery, drug development, diagnostics, pharmacoproteomics,
 CC agricultural biotechnology and structural bioinformatics, and especially
 CC in immunological assays for determining epitope expression. The methods
 CC of the invention are readily automatable, rapid, reproducible,
 CC quantifiable, and provide accurate results, and allows simultaneous
 CC analysis of multiple epitopes, with improved sensitivity and specificity.
 CC Sequences AAM52843-AAM52931 represent pentapeptides derived from the 19
 CC kD C-terminal region of Plasmodium falciparum merozoite surface protein 1
 CC (MSP1-19) that were used in epitope mapping according to the method of
 CC the invention
 XX
 XX Sequence 5 AA;
 SQ

KW Merozoite surface protein 1; MSP1-19; C-terminal region; epitope mapping;
 KW immunological assay; epitope expression; disease diagnosis;
 KW therapeutic target identification; drug discovery; development;
 KW binding activity determination; pharmacoproteomics;
 KW agricultural biotechnology; structural bioinformatics.
 XX
 OS Plasmodium falciparum.
 XX
 XX WO200188538-A2.
 XX
 XX PD 22-NOV-2001.
 XX
 XX PF 10-MAY-2001; 2001WO-US015450.
 XX
 XX PR 12-MAY-2000; 2000US-00569713.
 XX
 XX PA (DUMA/) DUMAS D P.
 XX
 XX PT Dumas DP;
 XX
 XX DR WPI; 2002-049548/06.
 XX
 FT A composition comprising reagent ligands attached to a solid support and
 PT reagent antibodies specifically bound to the ligands, useful in drug
 PT development, diagnostics and immunological assays for determining epitope
 PT expression.
 XX
 XX Example 1; Page 41; 55pp; English.
 XX
 CC The invention relates to compositions and methods for epitope mapping.
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 CC invention also encompasses a method for the determination of an epitope
 CC in a sample using the composition, and methods for diagnosing a disease,
 CC identifying a potential therapeutic target, mapping accessible epitopes
 CC of a polypeptide, and determining a binding activity in a sample. The
 CC composition of the invention may therefore be used in drug target
 CC discovery, drug development, diagnostics, pharmacoproteomics, and especially
 CC agricultural biotechnology and structural bioinformatics, and especially
 CC in immunological assays for determining epitope expression. The methods
 CC of the invention are readily automatable, rapid, reproducible,
 CC quantifiable, and provide accurate results, and allows simultaneous
 CC analysis of multiple epitopes, with improved sensitivity and specificity.
 CC Sequences AAM52843-AM52931 represent pentapeptides derived from the 19
 CC kD C-terminal region of Plasmodium falciparum merozoite surface protein 1
 CC (MSP1-19) that were used in epitope mapping according to the method of
 CC the invention
 XX
 XX SQ Sequence 5 AA;
 Query Match 75.0%; Score 21; DB 5; Length 5;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DKCL 4
 Db 1 DKCV 4
 |||:
 |||:
 RESULT 7
 ADM10126
 ID ADM10126 standard; peptide; 5 AA.
 XX
 XX AC ADM10126;
 XX
 XX DT 20-MAY-2004 (first entry)
 XX
 XX DE Human proteome unique recognition sequence (URS) seqid 450.
 KW soluble peptide analyte; unique recognition sequence; URS;
 KW protein detection; clinical diagnosis; environmental diagnosis;
 KW drug discovery; protein sequencing; pathogen detection; toxin detection;

KW anthrax toxin; small pox toxin; cholera toxin;
 KW packaged protein detection array; protein expression profile;
 KW drug screening; protein characterisation; disease prognosis;
 KW pathologic cell profiling; proteome epitope tag; human; proteome.
 XX
 OS Homo sapiens.
 XX
 XX US2004038307-A1.
 XX
 XX PD 26-FEB-2004.
 XX
 XX PF 12-MAY-2003; 2003US-00436549.
 XX
 XX PR 10-MAY-2002; 2002US-0379626P.
 PR 01-JUL-2002; 2002US-0393137P.
 PR 01-JUL-2002; 2002US-0393197P.
 PR 01-JUL-2002; 2002US-0393211P.
 PR 01-JUL-2002; 2002US-0393223P.
 PR 01-JUL-2002; 2002US-0393233P.
 PR 01-JUL-2002; 2002US-0393235P.
 PR 01-JUL-2002; 2002US-0393280P.
 PR 04-DEC-2002; 2002US-0430948P.
 PR 13-DEC-2002; 2002US-0433319P.
 XX
 XX PA (ENGE-) ENGNEOS INC.
 XX
 XX PI Lee PD, Meng X, Chan JW, Zhang S, Benkovic SJ;
 XX
 XX WPI; 2004-327083/30.
 XX
 DR Detecting proteins comprises providing solution of soluble peptide
 PT analytes, contacting solution with capture agents capable of interacting
 PT with unique recognition sequence of protein and detecting binding between
 PT agents and analytes.
 XX
 XX PS Claim 60; SEQ ID NO 450; 134pp; English.
 XX
 CC The invention describes a method of detecting proteins in sample. The
 CC method comprises: providing a solution of soluble peptide analytes
 CC produced by denaturation and/or cleavage of several sample proteins, and
 CC optionally, labeling the collection of peptides by a detectable part;
 CC contacting the solution with one or more capture agent(s), where each of
 CC the capture agent(s) is able to specifically recognise and interact with
 CC a unique recognition sequence (URS) of a reference protein; and detecting
 CC the binding between one or more of the capture agent(s) and the peptide
 CC analytes, where the detection of binding between a capture agent and a
 CC peptide analyte indicates the presence of the reference protein in the
 CC several of sample proteins. Also described are; and a method of
 CC quantifying proteins in a biological sample; a method of simultaneously
 CC detecting several specific proteins in a multi-protein sample. The method
 CC of the invention is used in clinical or environmental diagnosis, drug
 CC discovery, protein sequencing and for the detection of a pathogen or
 CC toxins (such as anthrax toxin, small pox toxin, and cholera toxin). A
 CC packaged protein detection array is useful for: quantifying various forms
 CC of post-translationally modified proteins in a biological sample;
 CC screening large libraries of natural or synthetic compounds to identify
 CC competitors of natural or non-natural ligands for the capture agent,
 CC which may be of diagnostic, prognostic, therapeutic or scientific
 CC interest; and to study the relationship between a subject protein
 CC expression profile and that subjects response to a foreign compound or
 CC drug. The methods of assaying differential protein expression are useful
 CC in the identification and validation of new potential drug targets as
 CC well as for drug screening. The capture agents are useful for protein
 CC characterisation, for screening, making prognosis of disease outcomes and
 CC providing treatment modality suggestion based on the profiling of the
 CC pathologic cells, prognosis of the outcome of a normal lesion and
 CC susceptibility of lesions to malignant transformation. The methods
 CC described are useful for identifying and/or detecting a specific organism
 CC based on the organisms proteome epitope tag. This is the amino acid
 CC sequence of a human proteome unique recognition sequence (URS).
 XX
 XX SQ Sequence 5 AA;

Query Match 75.0%; Score 21; DB 8; Length 5;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKCL 4
 Db 1 DRCL 4

RESULT 8
 ADR71292
 ID ADR71292 standard; peptide; 5 AA.
 AC ADR71292;
 XX
 XX 02-DEC-2004 (first entry)
 XX
 XX Human proteome epitope tag (PET) ENSP0000002594 #7.
 XX
 XX Human; Protein Epitope Tag; PET; post-translational modification;
 XX epitope; kinase; proteome; severe acquired respiratory syndrome; SARS.
 XX
 XX Homo sapiens.
 XX
 XX US2004180380-A1.
 XX
 XX 16-SEP-2004.
 XX
 XX 13-NOV-2003; 2003US-00712425.
 XX
 XX 10-MAY-2002; 2002US-0379626P.
 XX 01-JUL-2002; 2002US-0393137P.
 XX 01-JUL-2002; 2002US-0393137P.
 XX 01-JUL-2002; 2002US-0393211P.
 XX 01-JUL-2002; 2002US-0393223P.
 XX 01-JUL-2002; 2002US-0393233P.
 XX 01-JUL-2002; 2002US-0393235P.
 XX 01-JUL-2002; 2002US-0393280P.
 XX 04-DEC-2002; 2002US-0430948P.
 XX 13-DEC-2002; 2002US-0433319P.
 XX 12-MAY-2003; 2003US-00436549.
 XX
 XX (ENGE-) ENGINEOS INC.
 XX
 XX Lee FD, Meng X, Livingston D;
 XX WPI; 2004-675602/66.
 XX
 XX Detecting post-translational modification on target protein in sample, by
 XX generating capture agent using target fragment sequence with modification
 XX site and epitope tag, contacting sample with agent, detecting fragment
 XX bound to agent.
 XX
 XX Example 3; SEQ ID NO 450; 309pp; English.

The invention relates to detecting the presence of a post-translational modification on a target protein within a sample involving computationally analysing the amino acid sequence of the target protein to identify one or more candidate site for the post-translational modification, computationally identifying the amino acid sequence of one or more fragment of the target protein (where the fragment predictably results from a treatment of the target protein within the sample, and the fragment encompasses the potential post-translational modification site and a protein epitope tag (PET) unique to the fragment within the sample), generating a capture agent that specifically binds the PET, immobilising the capture agent to a support, subjecting the sample to the treatment to render the fragment soluble in solution, contacting the sample after the treatment to the capture agent and detecting in the fragment bound to the capture agent the presence or absence of the post-translational modification. Also included an array of capture agent for identifying all potential substrates of a kinase (or enzyme catalyzing a post-translational modification) within a proteome, identifying (M2), in a sample, a potential substrates of a kinase (or potential substrates of

an enzyme that catalyses a post-translational modification chosen from acetylation, amidation, deamidation, prenylation, formylation, glycosylation, hydroxylation, methylation, myristoylation, phosphorylation, ubiquitination, ribosylation and sulphation), an array of capture agents for determining which of a selected number of signal transduction pathways within a proteome is activated or inhibited in response to a stimulation, a business method for a biotechnology or pharmaceutical business (involving identifying one or more substrates for an enzyme catalysing a post-translational modification using (M2), optionally, verifying the post-translational modification of the substrates by the enzyme, and licensing to a third party the right to manufacture, or explore the use of the substrate as a target of the enzyme), a composition (CI) comprising several capture agents (where the several capture agents are collectively capable of specifically interacting with all potential substrates of a post-translational modification enzyme within an organisms proteome, and each of the capture agents is able to recognised and interact with only one PET within the potential substrate or its fragment containing the post-translational modification site), immunising a host animal against a disease condition associated with the presence or overexpression of a protein, generating antibodies specific for a marker protein for use in immunohistochemistry (involving computationally analysing the amino acid sequence of the marker protein to identify one or more PET(s) unique to the marker protein, where the PET(s) is located on the surface of marker protein), a method for simultaneous unambiguous detection quantification of a family of related proteins in a sample, processing a sample for use in PET-associated detection/quantitation of a target protein in the sample, a severe acquired respiratory syndrome (SARS) virus-specific PET amino acid sequence as given in the specification and generating antibodies specific for a PET sequence. The method is useful for detecting the presence of post-translational modification on a target protein within a sample obtained from human, mouse, rat, frog (Xenopus), fish (zebra fish), fly (Drosophila melanogaster), nematode (C. elegans), fission or budding yeast or plant (Arabidopsis thaliana). The method is useful for identifying a potential substrates of kinase or enzyme that catalyze a post-translational modification. The array is useful for identifying all potential substrates of a kinase or enzyme catalyzing post-translational modification within a proteome or for determining which of a selected number of signal transduction pathways within a sample from a proteome is activated or inhibited in response to a stimulation. The present sequence is a PET peptide of the invention.

Sequence 5 AA;
 Query Match 75.0%; Score 21; DB 8; Length 5;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKCL 4
 Db 1 DRCL 4

RESULT 9
 ADR95629
 ID ADR95629 standard; peptide; 5 AA.
 AC ADR95629;
 XX
 XX 16-JUN-2005 (first entry)
 XX
 XX Human peptide fragment, SEQ ID 450.
 XX
 XX Protein purification; epitope tagging.
 XX
 XX Homo sapiens.
 XX
 XX US2005069911-A1.
 XX
 XX 31-MAR-2005.
 XX
 XX 05-FEB-2004; 2004US-00773032.
 XX
 XX

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PR 10-MAY-2002; 2002US-0379626P.
PR 01-JUL-2002; 2002US-0393137P.
PR 01-JUL-2002; 2002US-0393137P.
PR 01-JUL-2002; 2002US-0393211P.
PR 01-JUL-2002; 2002US-0393211P.
PR 01-JUL-2002; 2002US-0393223P.
PR 01-JUL-2002; 2002US-0393223P.
PR 01-JUL-2002; 2002US-0393223P.
PR 01-JUL-2002; 2002US-0393235P.
PR 01-JUL-2002; 2002US-0393280P.
PR 04-DEC-2002; 2002US-0430948P.
PR 13-DEC-2002; 2002US-0433319P.
PR 12-MAY-2003; 2003US-00436549.
PR 13-NOV-2003; 2003US-00712425.
XX (ENGE-) ENGNEOS INC.
XX
XX Lee FD, Meng X, Afeyan NB;
XX
XX WPI; 2005-271962/28.
XX
XX Achieving highly accurate detection and quantitation of target protein in
XX sample, by contacting array of capture agents that selectively interact
XX with peptide epitope tag of target with polypeptide analytes and
XX detecting interaction.
XX
XX Example 3; SEQ ID NO 450; 311pp; English.
XX
XX The present invention relates to a method for achieving highly sensitive
XX detection and/or highly accurate quantitation of a target protein in a
XX sample. The method comprises providing different capture agents capable
XX of selectively interacting with peptide epitope tag (PET) of a target
XX protein as an addressable array, contacting the array with a solution of
XX polypeptide analytes, and detecting the presence and amount of target
XX protein in sample from interaction of polypeptide analytes with each
XX capture agents. The method is useful for detecting and/or quantitating a
XX target protein in a biological sample. The present sequence is one such
XX PET used to illustrate the invention.
XX
XX Sequence 5 AA;
SQ
Query Match 75.0%; Score 21; DB 9; Length 5;
Best Local Similarity 75.0%; Pred. No. 2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DKCL 4
Db 1 DRCL 4
RESULT 10
AAY73549
ID AAY73549 standard; peptide; 5 AA.
XX
XX AAY73549;
AC
XX
XX 07-MAR-2000 (first entry)
DT
XX
XX OB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:55.
DE
XX
XX Diagnosis; cancer; OB-cadherin; N-cadherin; E-cadherin; CAR; cyclic;
XX cell adhesion recognition sequence; leukaemia; metastasis;
XX prostate cancer; breast cancer; ovarian cancer; carcinoma.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO957565-A2.
XX
XX 11-NOV-1999.
XX
XX 05-MAY-1999; 99WO-CA000362.
XX
XX 05-MAY-1998; 98US-00073040.
XX
XX 06-NOV-1998; 98US-00187859.
XX
PR 20-JAN-1999; 99US-00234395.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Gour BJ, Byers S;
XX
XX WPI; 2000-062165/05.
XX
XX Detecting expression of OB-cadherin or N-cadherin used for diagnosing and
XX evaluating cancer.
XX
XX Disclosure; Page 18; 56pp; English.
XX
XX The present invention describes methods which have been developed for
XX detecting and evaluating cancer that are based on the finding that OB-
XX cadherin and N-cadherin are expressed by metastatic carcinoma cells, but
XX not by highly differentiated, poorly invasive carcinomas. A method for
XX determining the presence or absence of a cancer in a patient comprises:
XX (1) contacting a biological sample from the patient with a binding agent
XX that specifically binds to OB- or N-cadherin OR with an oligonucleotide
XX that hybridizes to a polynucleotide that encodes OB- or N-cadherin; and
XX (2) detecting in the sample an amount of polypeptide that binds to the
XX binding agent OR the amount of polynucleotide that hybridizes to the
XX oligonucleotide, relative to a predetermined cut-off value, and
XX determining the presence or absence of cancer in the patient from this.
XX The methods from the present invention can be used to determine the
XX metastatic potential of a cancer. The methods may be used to detect a
XX metastatic cancer in a patient, to monitor progression of a cancer, or to
XX evaluate the metastatic potential of a cancer. Cancers which may be
XX evaluated using the methods include leukemia, prostate cancer, breast
XX cancer and ovarian cancer. AAY73501 to AAY73813 represent peptide
XX sequences used in the exemplification of the present invention.
XX Specifically, AAY73503 to AAY73789 represent OB-cadherin cell adhesion
XX recognition (CAR) peptides and AAY73790 to AAY73808 represent N-cadherin
XX CAR peptides. AAY73906 to AAY73915 represent PCR primers used in examples
XX from the present invention
XX
XX Sequence 5 AA;
SQ
Query Match 71.4%; Score 20; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DKC 3
Db 3 DKC 5
RESULT 11
AAY60635
ID AAY60635 standard; peptide; 5 AA.
XX
XX AAY60635;
AC
XX
XX 02-MAR-2000 (first entry)
DT
XX
XX OB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:669.
DE
XX
XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
XX inhibition; cadherin extracellular domain; cell adhesion recognition;
XX OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
XX cadherin-14; cadherin-15; T-cadherin; P9-cadherin;
XX cadherin related neuronal receptor; LI-cadherin; protocadherin;
XX desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
XX rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
XX neurological disease; cyclic.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Disulfide-bond 1.5

```

PN WO9957149-A2.
 XX 11-NOV-1999.
 PD
 XX
 PF 05-MAY-1999; 99WO-CA000363.
 XX
 PR 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Gour BJ, Byers S;
 XX
 DR WPI; 2000-038791/03.
 XX
 XX New cadherin modulating agents, used for modulating nonclassical cadherin
 PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 PS Claim 18; Page 159; 252pp; English.
 XX
 CC The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MA can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention
 XX
 PS Sequence 5 AA;
 XX
 Query Match 71.4%; Score 20; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DKC 3
 Db 3 DKC 5
 RESULT 12
 AAB72592
 ID AAB72592 standard; peptide; 5 AA.
 XX
 AC AAB72592;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Thrombin-induced platelet activator antagonist #31.
 XX
 XX Platelet aggregation inhibitor; thrombin activation inhibitor;
 KW protease activated receptor 1; PAR1; platelet activation inhibitor;
 KW thrombosis; acute coronary syndrome.
 XX
 OS Unidentified.

XX WO200112656-A1.
 XX 22-FEB-2001.
 PD
 XX
 PF 17-AUG-2000; 2000WO-US040669.
 XX
 PR 17-AUG-1999; 99US-00375808.
 XX
 PA (THRO-) THROMGEN INC.
 XX
 PI Schmaier AH, Hasan AAK;
 XX
 DR WPI; 2001-226546/23.
 XX
 XX Inhibiting thrombin activation in human cell expressing protease
 PT activated receptor 1 (PAR1), comprises contacting mixtures of thrombin
 PT and human cell expressing PAR1, with a peptide that inhibits platelet
 PT activation.
 XX
 PS Claim 5; Page 25; 49pp; English.
 XX
 CC The present invention relates to a method for inhibiting thrombin
 CC activation in a human cell expressing protease activated receptor 1
 CC (PAR1). The method involves using peptides (e.g. the present peptide)
 CC that inhibit platelet activation. The method is useful for preventing
 CC thrombosis and platelet aggregation. The method can be used for patients
 CC with acute coronary syndromes (e.g. crescendo angina, myocardial
 CC infarction) and for individuals who have acute coronary syndromes and
 CC receive percutaneous transluminal coronary angioplasty with an article
 CC stent placement
 XX
 PS Sequence 5 AA;
 XX
 Query Match 71.4%; Score 20; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DKC 3
 Db 3 DKC 5
 RESULT 13
 AAM52879
 ID AAM52879 standard; peptide; 5 AA.
 XX
 AC AAM52879;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Plasmodium falciparum MSP1-19 peptide #37, used in epitope mapping.
 XX
 KW Merozoite surface protein 1; MSP1-19; C-terminal region; epitope mapping;
 KW immunological assay; epitope expression; disease diagnosis;
 KW therapeutic target identification; drug discovery; development;
 KW binding activity determination; pharmacoproteomics;
 KW agricultural biotechnology; structural bioinformatics.
 XX
 OS Plasmodium falciparum.
 XX
 PN WO200188538-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-US015450.
 XX
 PR 12-MAY-2000; 2000US-00569713.
 XX
 PA (DUMA/) DUMAS D P.
 XX
 PI Dumas DP;
 XX

DR WPI; 2002-049548/06.

XX A composition comprising reagent ligands attached to a solid support and

PT reagent antibodies specifically bound to the ligands, useful in drug

PT development, diagnostics and immunological assays for determining epitope

PT expression.

XX Example 1; Page 41; 55pp; English.

XX The invention relates to compositions and methods for epitope mapping.

CC The invention encompasses a composition comprising a diverse population

CC of reagent ligands attached to a solid support and a diverse population

CC of reagent-specific antibodies specifically bound to the ligands. The

CC invention also encompasses a method for the determination of an epitope

CC in a sample using the composition, and methods for diagnosing a disease,

CC identifying a potential therapeutic target, mapping accessible epitopes

CC of a polypeptide, and determining a binding activity in a sample. The

CC composition of the invention may therefore be used in drug target

CC discovery, drug development, diagnostics, pharmacoproteomics, and especially

CC agricultural biotechnology and structural bioinformatics. The methods

CC in immunological assays for determining epitope expression. The methods

CC of the invention are readily automatable, rapid, reproducible,

CC quantifiable, and provide accurate results, and allows simultaneous

CC analysis of multiple epitopes, with improved sensitivity and specificity.

CC Sequences AAM52843-AAM52931 represent pentapeptides derived from the 19

CC kD C-terminal region of Plasmodium falciparum merozoite surface protein 1

CC (MSP1-19) that were used in epitope mapping according to the method of

CC the invention

XX Sequence 5 AA;

SQ

Query Match 71.4%; Score 20; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKC 3

Db |||

3 DKC 5

RESULT 14

ABG92247

ID ABG92247 standard; peptide; 5 AA.

XX

AC ABG92247;

XX

29-NOV-2002 (first entry)

XX

OB-cadherin CAR peptide #43.

XX

Cancer metastasis; osteoblast cadherin; OB-cadherin CAR; cytostatic;

KW protein therapy.

XX

Synthetic.

XX

US6433149-B1.

PN

13-AUG-2002.

XX

05-MAY-1999; 99US-00305927.

XX

05-MAY-1998; 98US-00073040.

PR

06-NOV-1998; 98US-00187859.

PR

20-JAN-1999; 99US-00234395.

PR

08-MAR-1999; 99US-00264516.

XX

(ADHE-) ADHEREX TECHNOLOGIES INC.

PA

Blaschuk OW, Symonds JM, Byers S, Gour BJ;

PI

WPI; 2002-681212/73.

XX

Inhibiting cancer metastasis, and the use of osteoblast (OB)-cadherin

PT

peptides, and antibodies that bind them, to inhibit adhesion and

PT metastasis of circulating cancer cells.

XX Disclosure; Fig 2; 82pp; English.

PS

The present invention relates to new methods for inhibiting cancer

CC metastasis, and the use of osteoblast (OB)-cadherin peptides, and

CC antibodies that bind them, to inhibit adhesion and metastasis of

CC circulating cancer cells. The methods of the invention are used to

CC inhibit cancer metastasis. The present amino acid sequence represents an

CC OB-cadherin CAR peptide, as described in the invention

XX Sequence 5 AA;

SQ

Query Match 71.4%; Score 20; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKC 3

Db |||

3 DKC 5

RESULT 15

ABU55761

ID ABU55761 standard; peptide; 5 AA.

XX

AC ABU55761;

XX

21-MAR-2003 (first entry)

XX

OB-cadherin cell adhesion recognition sequence peptide analogue #7.

DE

OB-cadherin; cell adhesion recognition; CAR; cytostatic; vulvular;

XX

OB-cadherin mediated cell adhesion; cyclization; central nervous system;

KW cancer; metastasis; tumour; blood vessel regression; wound healing;

KW vasopermeability; cell adhesion modulation; cyclic.

XX

Unidentified.

OS

US6472367-B1.

PN

29-OCT-2002.

XX

05-MAY-1998; 98US-00073040.

XX

05-MAY-1998; 98US-00073040.

PR

(ADHE-) ADHEREX TECHNOLOGIES INC.

PA

Blaschuk OW, Symonds JM, Gour BJ;

PI

WPI; 2003-165425/16.

XX

Novel cell adhesion modulating agent useful for e.g. modulating cell

PT adhesion of OB-cadherin-expressing cells and enhancing the delivery of a

PT drug to a tumor, comprises a native OB-cadherin cell adhesion recognition

PT sequence.

XX

Disclosure; Fig 3B; 42pp; English.

PS

The invention relates to a cell adhesion modulating agent comprising a

CC peptide four to nine amino acids in length that detectably inhibits OB-

CC cadherin mediated cell adhesion, consisting of a native OB-cadherin cell

CC adhesion recognition (CAR) sequence that comprises the sequence DDK and

CC optionally a residue on one or both sides of the CAR sequence to

CC facilitate cyclization. The modulating agent is useful for modulating

CC cell adhesion of OB-cadherin-expressing cells and for enhancing the

CC delivery of a drug to a tumor or to the central nervous system in a

CC mammal. The agent is also useful for treating cancer and/or inhibiting

CC invasion and metastasis of a cancer. The agent is further useful for

CC stimulating blood vessel regression, for enhancing wound healing in a

CC mammal, for enhancing adhesion of foreign tissue implanted within a

CC mammal, for increasing vasopermeability in a mammal, for disrupting cell
 CC adhesion mediated by multiple adhesion molecules, to facilitate cell
 CC identification, sorting in vitro or imaging in vivo and for permitting
 CC the selection of cells expressing OB-cadherin. This sequence represents
 CC an OB-cadherin CAR sequence cyclic peptide analogue, used as a cell
 CC adhesion modulating agent
 XX
 SQ Sequence 5 AA;

Query Match 71.4%; Score 20; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKC 3
 |||
 Db 3 DKC 5

Search completed: January 11, 2006, 15:32:48
 Job time : 131 secs

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November 2005

Published_Applications_Nucleic_Acid_and_Published_Applications_Amino_Acid_database searches now generate two sets of results each. The Published_Applications_databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New_databases; older published applications make up the Published_Applications_Main_databases.

Searches run against Nucleic_Acid_Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino_Acid_Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSs have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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